

Figure 1

	<u>Gene symbol</u>	<u>Gene name</u>
5	OSBP	Oxysterol-binding protein
	NFKB3 (p65)	nuclearfactor of kappa light polypeptide gene enhancer B-cells 3
10	CAPN1	Calpain, large polypeptide L1
	CCND1	Cyclin D1
15	EFEMP2*	EGF-containing fibulin-like extracellular matrix protein 2
	FOSL1	FOS-like antigen-1
	PLCB3	Phospholipase C, beta 3 (phosphatidylinositol-specific)
20	PPPICA	Protein phosphatase-1, catalytic subunit, alpha isoform
	VEGFB	Vascular endothelial growth factor B
25	ESRRA, ERR1	estrogen-related receptor alpha
	CTSW	Cathepsin W
	GALN*	Galanin
30	LRP5, LRP7, LR3*	Low density lipoprotein receptor-related protein-5
	CBP2	Collagen-binding protein 2 (colligen 2)
35	TCIRG1	T-cell immune regulator 1
	LTBP3	Latent transforming growth factor-beta binding protein-3
	FGF19*	Fibroblast growth factor 19 (FGF19)
40	Delta5-desaturase*	Delta5-desaturase

Figure 2

GCCATGGAGCCCCGAGTGAGCGCGCGCGGGCCCCGTCCGGCCGCGCGGACAACAT
 GGAGGCAGCGCCCGCCCGGGCCGCGCTGGCCGCTGCTGCTGCTGCTGCTGCT
 5 GCTGGCGCTGTGCGGCTGCCCCGGCCCCCGCGCGGGCCTCGCCGCTCCTGCTATTT
 GCCAACC GCCGGGACGTACGGCTGGTGGACGCGCGCGGAGTCAAGCTGGAGTC
 CACCATCGTGGTCAGCGGCCTGGAGGATGCGGCCGAGTGGACTTCCAGTTTTTC
 CAAGGGAGCCGTGTACTGGACAGACGTGAGCGAGGAGGCCATCAAGCAGACCT
 ACCTGAACCAGACGGGGGCGCCCGTGCAGAACGTGGTCATCTCCGGCCCTGGTCT
 10 CTCCCGACGGCCTCGCCTGCGACTGGGTGGGCAAGAAGCTGTACTGGACGGACT
 CAGAGACCAACCGCATCGAGGTGGCCAACCTCAATGGCACATCCCGGAAGGTGC
 TCTTCTGGCAGGACCTTGACCAGCCTAGGGCCATCGCCTTGGACCCCGCTCAGG
 GGTACATGTACTGGACAGACTGGGGTGAGACGCCCCGGATTGAGCGGGCAGGG
 ATGGATGGCAGCACCCGGAAGATCATTGTGGACTCGGACATTTACTGGCCCAAT
 15 GGACTGACCATCGACCTGGAGGAGCAGAAGCTCTACIGGGCTGACGCCAAGCTC
 AGCTTCATCCACCGTGCCAACCTGGACGGCTCGTTCCGGCAGAAGGTGGTGGAG
 GGCAGCCTGACGCACCCCTTCGCCCTGACGCTCTCCGGGGACACTCTGTACTGG
 ACAGACTGGCAGACCCGCTCCATCCATGCCTGCAACAAGCGCACTGGGGGGAAG
 AGGAAGGAGATCCTGAGTGCCCCICTACTACCCCATGGACATCCAGGTGCTGAGC
 20 CAGGAGCGGCAGCCTTTCTTCCACACICCGCIGTGAGGAGGACAAIGCGGGCTGC
 TCCACCTGTGCTGCTGTCCCCAAGCGAGCCTTCTACACATGCGCCIGCCCCA
 CGGGTGTGCAGCTGCAGGACAACGGCAGGACGIGTAAGGCAGGAGCCGAGGAG
 GTGCTGCTGCTGGCCCCGGCGGACGGACCIACGGAGGATCTCGCTGGACACGCCG
 GACTTCACCGACATCGTGCTGCAGGTGGACGACAICCGGCACGCCAITGCCATC
 25 GACTACGACCCGCTAGAGGGCTATGTCTACTGGACAGATGACGAGGIGCGGGCC
 ATCCGCAGGGCGTACCTGGACGGGTCTGGGGCGCAGACGCTGGTCAACACCGGAG
 ATCAACGACCCCGATGGCATCGCGGICGACTGGGTGGCCCCGAAACCTCTACTGG
 ACCGACACGGGCACGGACCGCATCGAGGTGACGCGCCTCAACGGCACCTCCCGC
 AAGATCCTGGTGTGCGGAGGACCTGGACGAGCCCCGAGCCAICGCACTGCACCCC
 30 GTGATGGGCCTCATGTACTGGACAGACTGGGGAGAGAACCTAAAATCGAGTGT
 GCCAACTTGGATGGGCAGGAGCGGGCIGTGCTGGTCAATGCCICCCICGGGTGG
 CCCAACGGCCTGGCCCTGGACCTGCAGGAGGGGAAGCCTACTGGGGAGACGCC
 AAGACAGACAAGATCGAGGTGATCAATGTTGATGGGACGAAGAGGCGGACCCT
 CTTGGAGGACAAGCTCCCGCACATTTTCGGGTTCACGCTGCTGGGGGACTTCAT
 35 CTACTGGACTGACTGGCAGCGCCGACGATCGAGCGGGTGCACAAGGTCAAGGC
 CAGCCGGGACGTATCATTTGACCAGCTGCCCCGACCTGATGGGGCICAAAGCTGT
 GAATGTGGCCAAGGTGCTCGGAACCAACCCGCTGTGCGGACAGGAACGGGGGGT
 GCAGCCACCTGTGCTTCTTACACCCCCACGCAACCCGGTGTGGCTGCCCATCG
 GCCTGGAGCTGCTGAGTGACATGAAGACCTGCATCGTGCCTGAGGCCTTCTTGG
 40 TCTTACCAGCAGAGCCGCCATCCACAGGATCTCCCTCGAGACCAATAACAACG
 ACGTGGCCATCCCGCTCACGGGCGTCAAGGAGGCCTCAGCCCTGGACTTTGATG
 TGTCACAACACATCTACTGGACAGACGTACGCTGAAGACCATCAGCCGCG
 CCTTCATGAACGGGAGCTCGGTGGAGCACGTGGTGGAGTTTGGCCTTGACTACC
 CCGAGGGCATGGCCGTTGACTGGATGGGCAAGAACCTCTACTGGGCCGACACTG
 45 GGACCAACAGAATCGAAGTGGCGCGGCTGGACGGGCAGTTCCGGCAAGTCCTC
 GTGTGGAGGGACTTGGACAACCCGAGGTGCTGGCCCTGGATCCACCAAGGGC
 TACATCTACTGGACCGAGTGGGGCGGCAAGCCGAGGATCGTGCGGGCCTTCATG

2010201547550

Figure 2 (Page 2 of 3)

GACGGGACCAACTGCATGACGCTGGTGGACAAGGTGGGCGGGCCAAACGACCT
CACCATTGACTACGCTGACCAGCGCCTCTACTGGACCGACCTGGACACCAACAT
GATCGAGTCGTCCAACATGCTGGGTGAGGAGCGGGTCGTGATTGCCGACGATCT
CCCGCACCCGTTCCGTCTGACGCAGTACAGCGATTATATCTACTGGACAGACTG
5 GAATCTGCACAGCATTGAGCGGGCCGACAAGACTAGCGGCCGGAACCGCACCCCT
CATCCAGGGCCACCTGGACTTCGTGATGGACATCCTGGTGTTCCTCCTCCC
CAGGATGGCCTCAATGACTGTATGCACAACAACGGGCAGTGTGGGCAGCTGTGC
CTTGCCATCCCCGGCGGCCACCGCTGCGGCTGCGCCTCACACTACACCCTGGAC
CCCAGCAGCCGCAACTGCAGCCCCGCCACACCTTCTTGCTGTTTCAGCCAGAAA
10 TCTGCCATCAGTCGGATGATCCCGGACGACCAGCACAGCCCCGGATCTCATCCTG
CCCCTGCATGGACTGAGGAACGTCAAAGCCATCGACTATGACCCACTGGACAAG
TTCATCTACTGGGTGGATGGGCGCCAGAACATCAAAGCGAGCCAAGGACGACGG
GACCCAGCCCTTTGTTTTGACCTCTCTGAGCCAAAGGCCAAAACCCAGACAGGCA
GCCCCACGACCTCAGCATCGACATCTACAGCCGGACACTGTTCTGGACGTGCGA
15 GGCCACCAATACCATCAACGTCCACAGGCTGAGCGGGGAAGCCATGGGGGTGG
TGCTGCGTGGGGACCGCGACAAGCCCAGGGCCATCGTCGTCAAACGCGGAGCGA
GGGTACCTGTACTTCACCAACATGCAGGACCGGGCAGCCAAGATCGAACGCGCA
GCCCTGGACGGCACCGAGCGCGAGGTCTCTTACCACCGGCCCTCATCCGCCCT
GTGGCCCTGGTGGTGGACAACAACACTGGGCAAGCTGTTCTGGGTGGACGCGGAC
20 CTGAAGCGCATTGAGAGCTGTGACCTGTGAGGGGCCAACCGCCTGACCCTGGAG
GACGCCAACATCGTGCAGCCTCTGGGCCTGACCATCCTTGGCAAGCATCTCTAC
TGGATCGACCGCCAGCAGCAGATGATCGAGCGTGTGGAGAAGACCACCGGGGA
CAAGCGGACTCGCATCCAGGGCCGTGTGCCCCACCTCACTGGCATCCATGCAGT
GGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCACCCATGTGCCCGTGACAATGG
25 TGGCTGCTCCCATCTGTATTGCCAAGGGTGATGGGACACCACGGTGCTCATG
CCCAGTCCACCTCGTGCTCCTGCAGAACCTGCTGACCTGTGGAGAGCCGCCAC
CTGCTCCCCGGACCAAGTTTGCATGTGCCACAGGGGAGATCGACTGTATCCCCGG
GGCCTGGCGCTGTGACGGCTTTCCCGAGTGCGATGACCAGAGCGACGAGGAGGG
CTGCCCCGTGTGCTCCGCCGCCAGTTCCCTGCGCGCGGGGTCAGTGTGTGA
30 CCTGCGCCTGCGCTGCGACGGCGAGGCAGACTGTCAGGACCGCTCAGACGAGGC
GGACTGTGACGCCATCTGCCTGCCCAACCAGTTCCGGTGTGCGAGCGGCCAGTG
TGTCCTCATCAAACAGCAGTGCGACTCCTTCCCCGACTGTATCGACGGCTCCGA
CGAGCTCATGTGTGAAATCACCAAGCCGCCCTCAGACGACAGCCCCGGCCACAG
CAGTGCCATCGGGCCCCGTCAATTGGCATCATCCTCTCTCTCTTCGTGATGGGTGGT
35 GTCTATTTTGTGTGCCAGCGCGTGGTGTGCCAGCGCTATGCGGGGGCCAAACGGG
CCCTTCCCGCACGAGTATGTGACGGGACCCCGCACGTGCCCCCTCAATTTATA
GCCCCGGGCGGTTCCAGCATGGCCCCCTTACAGGCATCGCATGCGGAAAGTCC
ATGATGAGCTCCGTGAGCCTGATGGGGGGCGGGGCGGGGTGCCCCCTGTACGAC
CGGAACCACGTACAGGGGGCCTCGTCCAGCAGCTCGTCCAGCACGAAGGCCACG
40 CTGTACCCGCCGATCCTGAACCCGCCGCCCTCCCCGGCCACGGACCCCTCCCTG
TACAACATGGACATGTTCTACTCTTCAAACATTCCGGCCACTGCGAGACCGTAC
AGGCCCTACATCATTGAGGAATGGCGCCCCCGACGACGCCCTGCAGCACCGGAC
GTGTGTGACAGCGACTACAGCGCCAGCCGCTGGAAGGCCAGCAAGTACTACCTG
GATTTGAACTCGGACTCAGACCCCTATCCACCCCCACCCACGCCCCACAGCCAG
45 TACCTGTGCGCGGAGGACAGCTGCCCCGCCCTGCCCCGCCACCGAGAGGAGCTAC
TTCCATCTCTTCCCGCCCCCTCCGTCCCC
CTGCACGGACTCATCCTGACCTCGGCCGGGCCACTCTGGCTTCTCTGTGCCCCCTG
TAAATAGTTTTAAATATGAACAAAGAAAAAATATATTTTATGATTTAAAAAAT

AAATATAATTGGGATTTTAAAAACATGAGAAATGTGAACTGTGATGGGGTGGGC
AGGGCTGGGAGAACTTTGTA

Figure 3

MEAAPPGPPWPLLLLLLLLLLALCGCPAPAAASPLLLFANRRDVRLVDAGGVKLESTI
VVSGLDAAAVDFQFSKGAVYWTDVSEEAIKQTYLNQTGAAYQNVVISGLVSPDGL
5 ACDWVGKKLYWTDSETNRIEVANLNGTSRKVLFWQDLQDQPRALDPAHGYMYW
TDWGETPRIERAGMDGSTRKIIVDSDIYWPNGLTIDLEEQLYWADAKLSFIHRANL
DGSFRQKVVEGSLTHPFALTLSGDTLYWTDWQTRSIHACNKRTGGKRKEILSALYSP
MDIQVLSQERQPFHTRCEEDNGGCSHLCLLSPSEPFYTCACPTGVQLQDNGRTCKA
GAEVLLLARRTDLRRISLDTPDFTDIVLQVDDIRHALAIDYDPLEGYVYWTDDEVR
10 AIRRAYLDGSGAQLVNTENDPDGIAVDWVARNLYWTDGTGTDRIEVTRLNGTSRK
ILVSEDLDEPRALALHPVMGLMYWTDWGENPKIECANLDGQERRVLVNASLGWPN
GLALDLQEGKLYWGDAKTDKIEVINVDGTKRRTLLEDKLPHFIFTLLGDFIYWTD
WQRRSIERVHKVKASRDVIIDQLPDLMLGKAVNVAKVVGTPNPNADRNGGCSHLCHF
TPHATRCGCPGLELLSDMKTCTVPEAFLVFTSRAAIHRISLETNNNDVAIPLTGVKE
15 ASALDFDVSNHHIYWTDVSLKTISRANMNGSSVEHVVEFGLDYPEGMAVDWMGKN
LYWADTGTNRIEVARLDGQFRQVLVWRDLNPRSLALDPTKGYTYWTEWGGKPRI
VRAFMDGTNCMTLVKVGANDLTIDYADQRLYWTDLDTNMIESSNMLGQERVV
IADDLPHPFGLTQYSDIYWTDWNLHSIERADKTSGRNRTLIQGHLDVMDILVFHS
SRQDGLNDCMHNNNGQCGQLCLAIPEGHRCGCASHYTLDPSSRNCSPPTTFLFSQKS
20 AISRMIPDDQHSPDLILPLHGLRNVKAIDYDPLDKFIYWVDGRQNIKRAKDDGTQPF
VLTSLSQGQNPDRQPHDLSDIYSRTLFWTCEATNTINVHRLSGEAMGVVLRGDRDK
PRAIVVNAERGYLYFTNMQDRAAKIERAALDGTREVLFTTGLIRPVALVVDNTLG
KLFVVDADLKRIESCDLSGANRLTLEDANIVQPLGLTILGKHLWIDRQQQMIEERVE
KTTGDKRTRIQRVAHLTGIIHAVEEVSLEEFSAHPCARDNGGCSHICIAKGDGTPRC
25 SCPVHLVLLQNLCTCEPPTCSPDQFACATGEIDCIPGAWRCDGFPECDDQSDEEGC
PVCSAAQFPCARGQCVDLRLRCDGEADCQDRSDEADCDAICLPNQFRCASGQCVLI
KQQCDSFPDCIDGSDELMCEITKPPSDDSPAHSSAIGPVIGIILSLFVMGGVYFVCQRV
VCQRYAGANGPFPHEYVSGTPHVPLNFIAPGGSQHGPFTGIACGKSMMSSVSLMGG
RGGVPLYDRNHVTGASSSSSSSTKATLYPPILNPPSPATDPSLYNMDMFYSSNIPAT
30 ARPYRPNIRGMAPPPTTPCSTDVCDSDYSASRWKASKYYLDLNSDSDPYPPPTPHSQ
YLSAEDSCPPSPATERSYFHLFPPPPSPCTDSS

Figure 4

Source	Nucleotide change	Protein change	Putative effect
OPS 88	G29A	Trp10stop	Truncation
Control	A459G	Pro153Pro	No change
Control	InsCTG33	Insert Leu at residue 12	Alters signal peptide
OPS 78	GACCTACG 1051-1058 ACCCTACA	AspLeuSer 351-353 ThrLeuLys	Unknown
OPS 59	C1282T	Arg428stop	Truncation
OPS 53	G1253T	Glu485stop	Truncation
OPS 23	delG1467	Frameshift	Truncation
OPS 82	G1481A	Arg494Gln	Unknown
OPS 2	C1708T	Arg570Trp	Unknown
OPS 72	G1999A	Val677Met	Unknown
OPS 45	insT2150	Frameshift	Truncation
OPS 41	G2202A	Trp734stop	Unknown
Control	C2220T	Asn740Asn	Unknown
OPS 92	delG2305	Frameshift	Truncation
OPS13	C2557T	Gln853stop	Truncation
OPS 7	delA3804	Frameshift	Truncation
OPS 53	C3989T	Ala1330Leu	Unknown
OPS 72	C3989T	Ala1330Leu	Unknown
Control	G4416T	Leu1472Leu	No change

Figure 5

NAME	SEQUENCE	LOCATION	PRODUCT SIZE
LRGEN1F	5'-TTG CTG CCC TAG ACT TAG CC-3'	-119	406
LRGEN1R	5'-CCA AGT CGC TTC CGA GAC-3'	+106	
LRGEN2F	5'-CAT CCC AGG GCT GTG TAT CT-3'	-65	543
LRGEN2R	5'-ACT TGG GCT CAT GCA AAT TC-3'	+81	
LRGEN3F1	5'-CCG ATG GGT GAG ATT TTA GG-3'	-118	329
LRGEN3R1	5'-CGT GGG TAC CTA CCG GAA C-3'	+16	
LRGEN4NF	5'-TAA TTG GGT CAG CAG CAA TG-3'	-72	277
LRGEN4NR	5'-GCA CTC ACA GAA AGG CTG-3'	+8	
LRGEN5NF	5'-AGT GAC GGT CCT CTT CTG GA-3'	-51	302
LRGEN5NR	5'-CAA GTG GAT CAT TTC GAA CG-3'	+120	
LRGEN6F	5'-TGG CTG AGT ATT TCC CTT GC-3'	-95	577
LRGEN6R	5'-CCA GAA TGA CAG GTC CAG GT-3'	+85	
LRGEN7F1	5'-TGC TTC TTC TCC AGC CTC AT-3'	-14	302
LRGEN7R1	5'-ATG TGG CCA AAT AGC AGA GC-3'	+116	
LRGEN8F	5'-GCA TTG AAC CCG TCT TGT TT-3'	-109	426
LRGEN8R	5'-GGC ACC TGA GCT CAA CAC TT-3'	+100	
LRGEN9F	5'-TGC TGG GCT GTT GT GTT TA-3'	-47	407
LRGEN9R	5'-CTT TGA GGC AGG AAC AGA GG-3'	+70	
LRGEN10F	5'-AGC GAA ACT CCG TCT CAA AA-3'	-79	417
LRGEN10R	5'-GCT CTA ATC ACT GAG GGC CA-3'	+110	
LRGEN11F1	5'-GAG GGC TGA GCT GAA GAG GT-3'	-105	398
LRGEN11R1	5'-CAG GTT GGG GAA CTT GCA G-3'	+108	
LRGEN12F	5'-ATT CAT GTG GTC GCT AGG CT-3'	-113	479
LRGEN12R	5'-GAA GCT CCT TTC AGC GTC AG-3'	+40	
LRGEN13F	5'-CCA GCT CCT CTG TGG CTT AC-3'	-57	352
LRGEN13R	5'-TCC TCC CTC TGC TAA GGA CA-3'	+95	
LRGEN14F	5'-CAG AGC TCT CCA GCC AGT G-3'	-149	440
LRGEN14R	5'-CTG TGA GAG GCT GGC ATT C-3'	+82	
LRGEN15NF	5'-ATG TGA CCT GTC AGC CTC G-3'	-131	415
LRGEN15NR	5'-TGC TGC CAT TAC TGA CAA TGA-3'	+83	
LRGEN16F	5'-TCT GTC CTC CCA AGC TGA GT-3'	-76	374
LRGEN16R	5'-CAC ACA GGA TCT TGC ACT GG-3'	+88	
LRGEN17F	5'-CAT GAG TTC TCA TTT GGC CC-3'	-92	321
LRGEN17R	5'-GCC ACA GGG ACT GTG ATT TT-3'	+103	
LRGEN18F	5'-CAA CTT CTG CTT TGA AGC CC-3'	-88	423
LRGEN18R	5'-CAG AGC CCC TAC TCC TGT GA-3'	+98	
LRGEN19F	5'-CCA GAC CTT GGT TGC TGT G-3'	-81	269
LRGEN19R	5'-CGT CTC CTC CCC TAA ACT CC-3'	+77	
LRGEN20NF	5'-ATG TTG GCC ACC TCT TTC TG-3'	-34	310
LRGEN20NR	5'-CTG CCT CCT CCA GAT CAT TC-3'	+39	
LRGEN21F	5'-GAG TCT CGT GGG TAG TGG GA-3'	-102	373

2020-09-26 14:55:00

Figure 5 (Page 2 of 2)

LRGEN21R	5'-AGA AAG CAA GCA TGC CTC AG-3'	+131	
LRGEN22F	5'-AGC CCT CTC TGC AAG GAA AG-3'	-96	305
LRGEN22R	5'-GCC CAC TAG CAC CCA GAA TA-3'	+111	
LRGEN23F	5'-GAC AGG CCT TTC CCG TTC-3'	-95	650
LRGEN23R	5'-CAG GAG GAC TCT CAT GGT GG-3'	+106	
LRCOD1F	5'-TTC GTC ATG GGT GGT GTC TA-3'	4192	416
LRCOD1R	5'-TTC CTC GAA TGA TGT AGG GC-3'	4607	
LRCOD2F	5'-ACC TGG ACT TCG TGA TGG AC-3'	2654	466
LRCOD2R	5'-CAG AAC AGT GTC CGG CTG TA-3'	3119	
LRCOD3F	5'-CCA TGG AGC CCG AGT GAG-3'	-50	504
LRCOD3R	5'-GTC AAG GTC CTG CCA GAA GA-3'	453	
LRCOD4F	5'-GGG CAA GAA GCT GTA CTG GA-3'	354	500
LRCOD4R	5'-TGG ATG TCC ATG GGT GAG TA-3'	853	
LRCOD5F	5'-CAG ACC CGC TCC ATC CAT-3'	767	484
LRCOD5R	5'-TCG TTG ATC TCG GTG TTG AC-3'	1250	
LRCOD6F	5'-ATC GAC TAC GAC CCG CTA GA-3'	1132	546
LRCOD6R	5'-GTA GAT GAA GTC CCC CAG CA-3'	1677	
LRCOD7F	5'-GCC AAG ACA GAC AAG ATC GAG-3'	1564	505
LRCOD7R	5'-TGT GGT TGT TGG ACA CAT CA-3'	2068	
LRCOD8F	5'-CAC AGG ATC TCC CTC GAG AC-3'	1966	522
LRCOD8R	5'-CTC GAT CAT GTT GGT GTC CA-3'	2487	
LRCOD9F	5'-CAG CCC TTT GTT TTG ACC TC-3'	3025	484
LRCOD9R	5'-TCC AGT AGA GAT GCT TGC CA-3'	3508	
LRCOD10F	5'-AAG CGC ATT GAG AGC TGT G-3'	3400	480
LRCOD10R	5'-CTC CTC GTC GCT CTG GTC-3'	3879	
LRCOD11F	5'-CAC AGG GGA GAT CGA CTG TAT-3'	3801	480
LRCOD11R	5'-ACA TAC TCG TGC GGG AAG G-3'	4280	
LRCOD12F	5'-GTC CAG CAG CTC GTC CAG-3'	4446	567
LRCOD12R	5'-TAC AAA GTT CTC CCA GCC CT-3'	5012	
LRCOD13F	5'-TCA TGG ACG GGA CCA ACT-3'	2369	431
LRCOD13R	5'-GGT GTA GTG TGA GGC GCA G-3'	2799	

2020-05-27 15:00:00

Figure 6

BMSR Construct Information

- 5 The following BSMR expression constructs have been constructed using the pcDNA3 expression vector for use in following BSMR expression, function, and other biological (e.g. ligand and downstream signaling) interactions.

- 10 1. A full length wild type construct extending from primers LRCOD3F to LRCOD12R.

- 15 Sequence encoding a FLAG antibody epitope (GAC TAC AAG GAC GAC GAT GAC AAG) was inserted into the wild-type construct immediately downstream of nucleotide 165 (relative to the "A" in the ATG translation start site). This construct expresses a BSMR protein which has a FLAG epitope between wild type BSMR amino acid residues 55 and 56.

This was accomplished using the following primer sequences and a Quickchange reaction:

- 20 LRPFLAGF: 5'-GAC TAC AAG GAC GAC GAT GAC AAG ACC ATC GTG GTC AGC GGC CTG-3'

- 25 LRPFLAGR: 5'-CTT GTC ATC GTC GTC CTT GTA GGA CTC CAG CTT GAC TCC GCC-3'

- 30 Sequence encoding a MYC antibody epitope (GAG CAG AAG CTG ATA TCC GAG GAG GAC CTG) was inserted immediately upstream of the stop codon after residue 4845 (relative to the "A" in the ATG translation start site). The construct expresses a BSMR protein which has a MYC epitope at the end of the wild type BSMR polypeptide.

This was accomplished using the following primer sequences and a Quickchange reaction:

- 35 LRPMYCF: 5'-GAG CAG AAG CTG ATA TCC GAG GAG GAC CTG TGA CCT CGG CCG GGC-3'

- LRPMYCR: 5'-CAG GTC CTC CTC GGA TAT CAG CTT CTG CTC GGA TGA GTC CGT GCA-3'

- 40 A expression construct containing both the FLAG and MYC antibody epitopes at the aforementioned sites has also been produced.

Figure 7

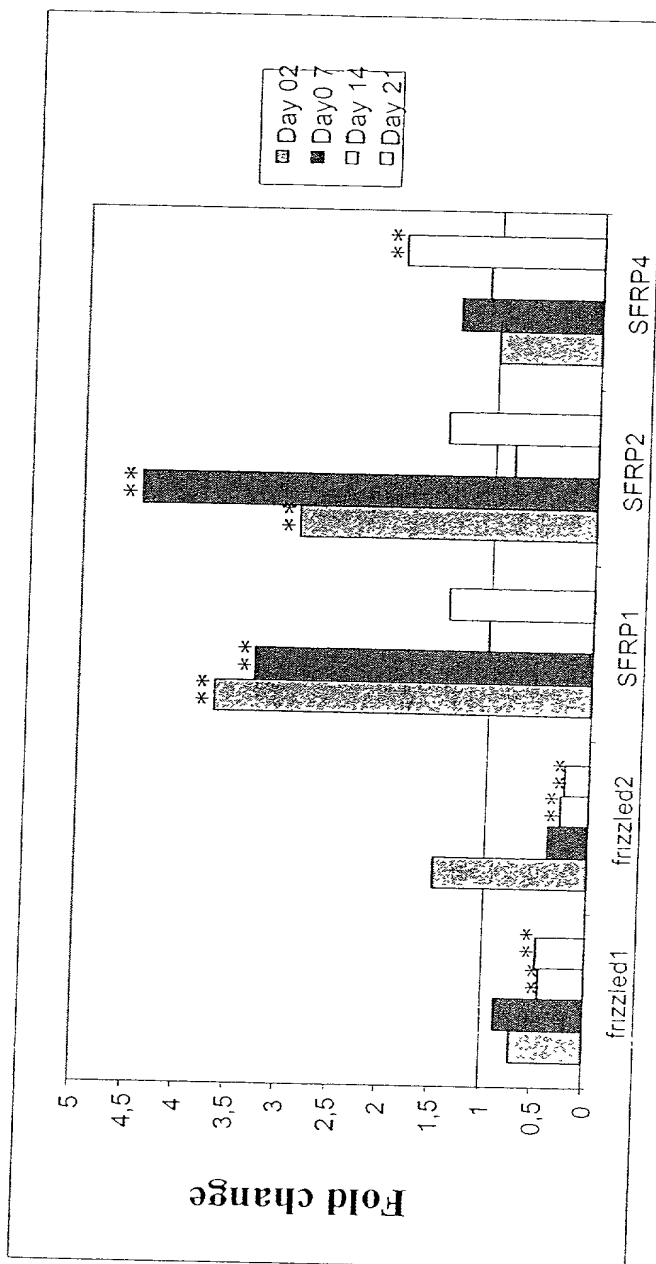


Figure 8

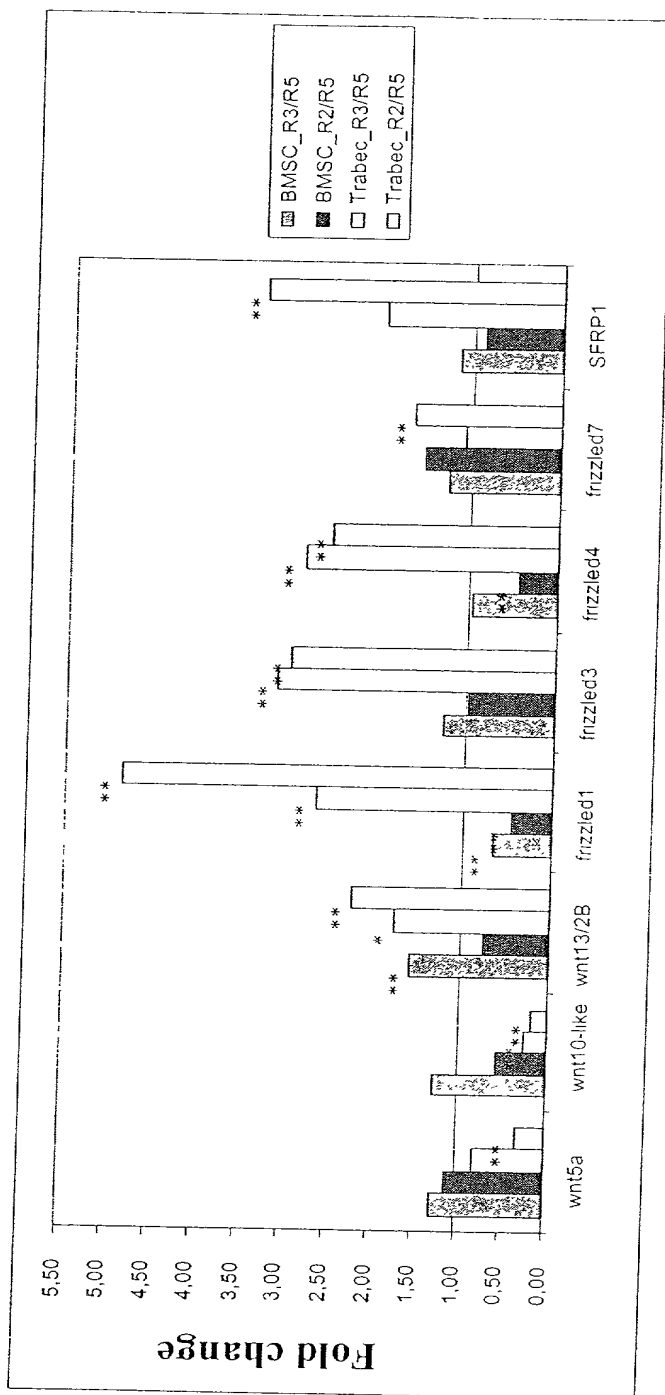


Figure 9

Cell line/treatment Gene name	C2C12/BMP2 (4 days)	C3H10T1/2/BMP2+SHH (4 days)	ST2/BMP2 (4 days)	MC3T3-E1 (3 days)
Frizzled1	2.25 x	NR	2.62x	2.11x
Frizzled4	NR	4.37x	NR	NR
SERP2/SARPI	8.10 x	0.5x (0.4x with SHH alone)	8.54x	3.61x (0.09 wth TGFbeta)

Figure 10

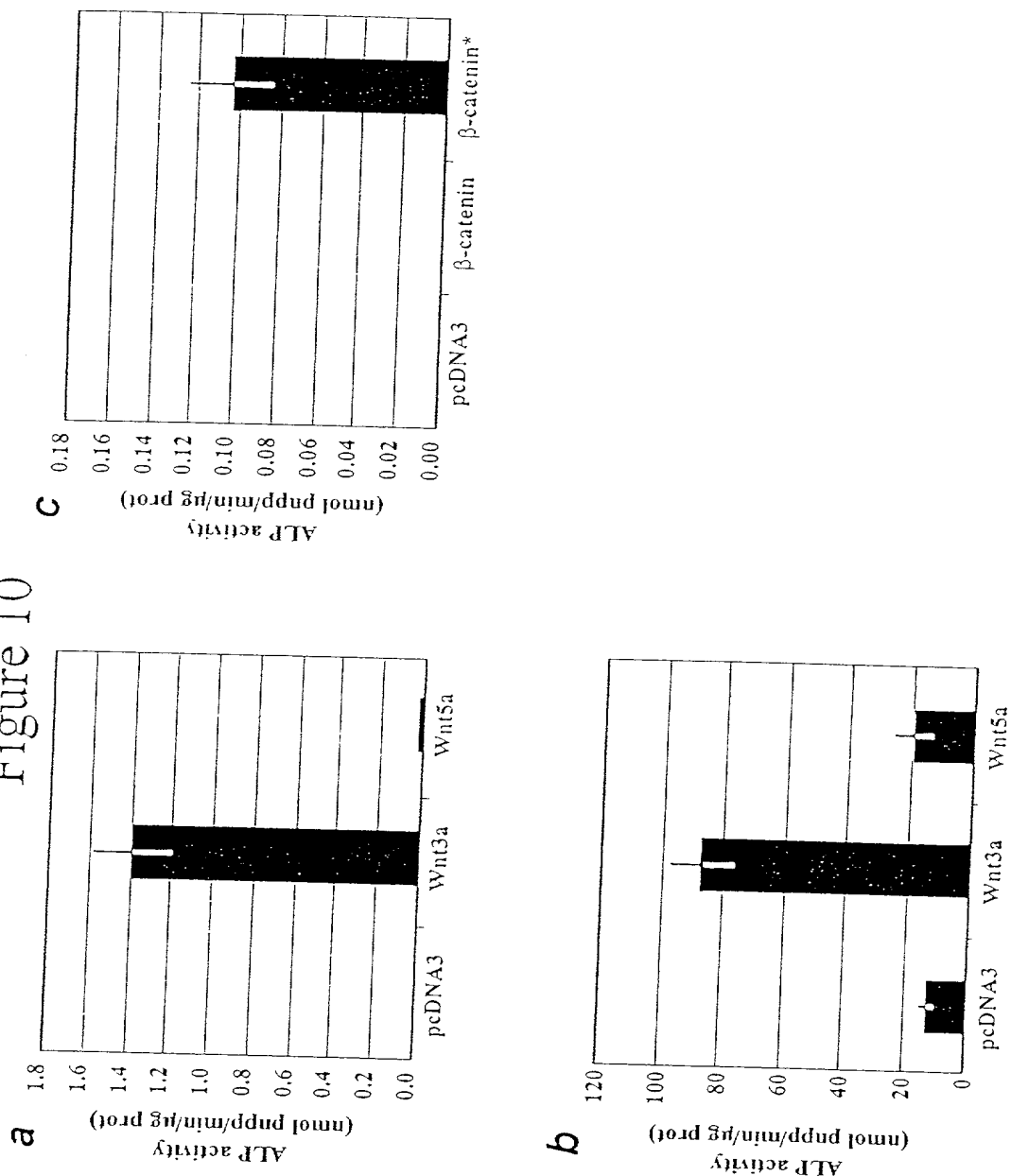
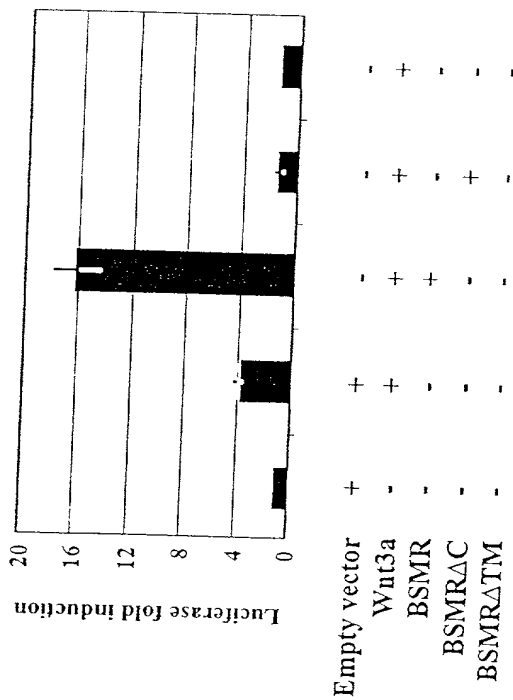
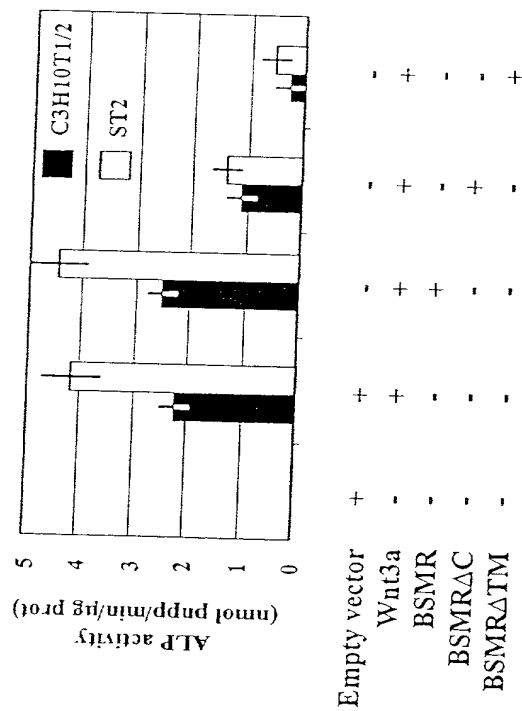


Figure 11

a



b



c

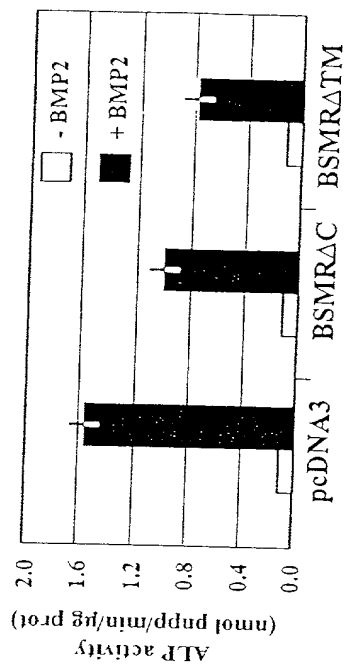


Figure 12

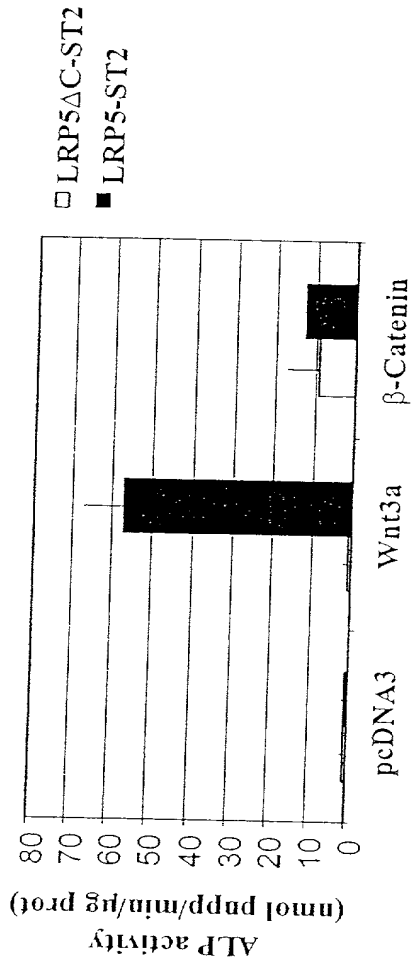


Figure 13

RVRLASHLRKLRK

RLTRKRGLKLA

CRAKRNNFKSA

LKWKS

KIRVKAGETQKKVIFCSREKVSHL

FIPLKPTVKMLERSNHVSRTEVSSNHV

DKGMAPALRHLYKELMGPWN

DALKLAIDNALSIT

2000-01-01